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SALMONELLA SECRETED PROTEINS AND USES THEREOF

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Background of the Invention

The invention relates to virulence factors of
10 *Salmonella typhimurium*.

Salmonella typhimurium (*S. typhimurium*) enter
epithelial cells by a process termed bacterial-mediated
endocytosis. *S. typhimurium* stimulates these normally
nonphagocytic cells to undergo significant cytoskeletal
15 rearrangements that are visualized as localized membrane
ruffling adjacent to the bacteria. Bacteria are then
internalized via membrane-bound vacuoles formed from the
membrane ruffles.

Several *S. typhimurium* loci have been identified
20 that are required for the induction of bacterial-mediated
endocytosis (BME) by epithelial cells. Many of these
epithelial-cell signaling loci have a similar chromosomal
location, clustered within a 40 kb "virulence island"
located between 59 and 60 minutes on the *S. typhimurium*
25 chromosome (Mills et al., *Mol. Microbiol.* 15:749-759,
1995). *InvJ* is a *S. typhimurium* gene which is thought
to encode a secreted protein necessary for BME (Collazo
et al., *Mol. Microbiol.* 15:25-38, 1995).

Summary of the Invention

30 The invention features proteins involved in
Salmonella typhimurium virulence and/or
bacterial-mediated endocytosis. The genes encoding these
proteins have now been cloned and their corresponding
gene products characterized. Accordingly, the invention

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features a substantially pure DNA encoding a *Salmonella* secreted protein (Ssp). By the term "*Salmonella* secreted protein" is meant a *Salmonella*-derived protein, the secretion of which is dependent on the expression of 5 PrgH. In preferred embodiments the invention features substantially pure DNA encoding a *Salmonella typhimurium* secreted protein. By *Salmonella typhimurium* secreted protein is meant as *Salmonella typhimurium* derived protein, the secretion of which is dependent on the 10 expression of PrgH.

One aspect of the invention features a substantially pure DNA molecule which includes the SspB gene; preferably, the DNA includes the DNA sequence of SEQ ID NO: 1, or degenerate variants thereof encoding the 15 amino acid sequence of SEQ ID NO: 5. In another aspect the invention features a substantially pure DNA molecule which includes the SspC gene; preferably, the DNA includes the DNA sequence of SEQ ID NO: 2, or degenerate variants thereof encoding the amino acid sequence of SEQ 20 ID NO: 6. In another aspect the invention features a substantially pure DNA molecule which includes the SspD gene; preferably, the DNA includes the DNA sequence of SEQ ID NO: 3, or degenerate variants thereof encoding the amino acid sequence of SEQ ID NO: 7. In another aspect 25 the invention features a substantially pure DNA molecule which included the SspA gene; preferably, the DNA includes the DNA sequence of SEQ ID NO: 4, or degenerate variants thereof encoding the amino acid sequence of SEQ ID NO: 8. The invention also features a substantially 30 pure DNA molecule which includes the SspB, SspC, SspD, and SspA genes; preferably, the DNA includes the DNA sequence of SEQ ID NO: 15. The invention also features a substantially pure DNA molecule which includes the SspH gene; preferably, the DNA includes the DNA sequence of 35 SEQ ID NO: 13, or degenerate variants thereof encoding

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the amino acid sequence of SEQ ID NO: 14. The invention also features a substantially pure DNA molecule which includes the *Salmonella tyrosine phosphatase A* (*stpA*) gene; preferably, the DNA includes the DNA sequence of 5 SEQ ID NO: 10, or degenerate variants thereof encoding the amino acid sequence of SEQ ID NO:12.

The invention also features a cell into which has been introduced substantially pure DNA encoding an *Ssp* (or a mutant variant thereof). The substantially pure 10 DNA can be introduced as a portion of a plasmid or other autonomously replicating molecule. In addition the substantially pure DNA can be introduced by homologous recombination. Preferably, the bacterial cell is a *Salmonella* cell; more preferably the bacterial cell is a 15 *Salmonella typhimurium* cell. Cells into which have been introduced substantially pure DNA encoding an *Ssp* (or mutant variant thereof) can be used as a source of purified *Ssp*.

The invention includes a substantially pure *SspC* 20 polypeptide, e.g., a polypeptide which includes an amino acid sequence substantially identical to the amino acid sequence of SEQ ID NO: 6 or an active fragment thereof and a substantially pure *SspD* polypeptide, e.g., a polypeptide which includes an amino acid sequence 25 substantially identical to the amino acid sequence of SEQ ID NO: 7 or an active fragment thereof. The invention includes a substantially pure *SspB* polypeptide, e.g., a polypeptide which includes an amino acid sequence substantially identical to the amino acid sequence of SEQ 30 ID NO: 5 (incomplete protein sequence) or an active fragment thereof and a substantially pure *SspA* polypeptide, e.g., a polypeptide which includes an amino acid sequence substantially identical to the amino acid sequence of SEQ ID NO: 8-(incomplete protein sequence) or 35 an active fragment thereof. The invention includes a

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substantially pure full-length SspB polypeptide, e.g., a polypeptide which includes an amino acid sequence substantially identical to the amino acid sequence of SEQ ID NO: 5 (incomplete protein sequence) and the remainder 5 of the SspB sequence. Full-length SspA and SspB genes can be isolated by those skilled in the art using the partial DNA sequences disclosed herein. The invention also includes a substantially pure full-length SspA polypeptide, e.g., a polypeptide which includes an amino 10 acid sequence substantially identical to the amino acid sequence of SEQ ID NO: 8 (incomplete protein sequence) and the remainder of the SspA sequence. The invention also features An active fragment of an Ssp B polypeptide or an SspC polypeptide or an SspD polypeptide is defined 15 as an SspB, SspC, or an SspD polypeptide, respectively, at least 50 amino acids, preferably at least 25 amino acids, more preferably at least 10 amino acids in length having the ability to induce BME in the absence of the full-length version of the corresponding protein. In 20 other preferred embodiments the SspB, SspC, SspD or SspA polypeptide is able to translocate into an epithelial cell, preferably a human epithelial cell. Translocation can be assayed using any suitable assay, e.g., the assay of Sogy et al. (*Molecular Microbiol.* 14:583:94, 1994).

25 The invention also includes a substantially pure SspH polypeptide, e.g., a polypeptide which includes an amino acid sequence substantially identical to the amino acid sequence of SEQ ID NO:14, or a biologically active fragment thereof.

30 The invention also includes a substantially pure IagB polypeptide, e.g., a polypeptide which includes an amino acid sequence substantially identical to the amino acid sequence of SEQ ID NO:11, or a biologically active fragment thereof.

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Also within the invention is an antibody which binds to a *Ssp*, e.g., a polyclonal or monoclonal antibody which specifically binds to an epitope of *Ssp*. Polyclonal and monoclonal antibodies produced against the 5 polypeptides of the invention can be used as diagnostic or therapeutic agents. The invention encompasses not only an intact monoclonal antibody, but also an immunologically-active antibody fragment, e.g., a Fab or (Fab)₂ fragment; an engineered single chain Fv molecule. 10 In preferred embodiments, the antibody may be linked to a detectable label, e.g. a radioactive label, fluorescent label, paramagnetic label, or colorimetric label.

The invention also includes a method of detecting a *Salmonella* infection in a mammal which includes the 15 steps of contacting a biological sample derived from the mammal, e.g., a human patient, with a *Ssp*-specific antibody and detecting the binding of the antibody to a *Ssp* in the sample. Antibody binding indicates that the mammal is infected with *Salmonella*. The presence of 20 *Salmonella* in a biological sample may also be detected using a method which includes the steps of contacting the sample with a *Ssp*-encoding DNA, or the complement thereof, under high stringency conditions and detecting the hybridization of the DNA to nucleic acid in the 25 sample. Hybridization indicates the presence of *Salmonella* in the biological sample. By "high stringency" is meant DNA hybridization and wash conditions characterized by high temperature and low salt concentration, e.g., wash conditions of 65°C at a salt 30 concentration of approximately 0.1 × SSC. For example, high stringency conditions may include hybridization at about 42°C in the presence of about 50% formamide; a first wash at about 65°C with about 2 × SSC containing 1% SDS; followed by a second wash at about 65°C with about 35 0.1 × SSC.

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The invention also features a method for detecting the presence of antibodies to an Ssp using all or part of an Ssp protein. The method includes contacting a biological sample with the Ssp protein and measuring the 5 binding of the Ssp protein to an antibody present in the sample.

The invention also features a method of targeting an antigen to an epithelial cell in a mammal which includes the steps of linking the antigen to an Ssp, 10 e.g., SspC or SspD, or active fragment thereof, to produce a Ssp chimeric antigen and administering the chimeric antigen to the mammal.

A method of inducing a cytotoxic T cell immune response in a mammal is also within the invention. This 15 method includes the steps of linking the antigen to an Ssp or active fragment thereof to produce a Ssp chimeric antigen and contacting an antigen-presenting cell, e.g., a Class I major histocompatibility complex (MHC) antigen-expressing cell, with the chimeric antigen.

20 The invention also features a vaccine which includes a bacterial cell, the virulence of which is attenuated by decreased secretion of a Ssp, and a method of vaccinating an mammal, e.g., a human patient, against a *Salmonella* infection by administering such a vaccine.

25 Preferably, the bacterial cell is a *Salmonella typhimurium* cell, e.g., a *Salmonella enteriditis* cell, or a *Salmonella typhi* cell. A live *Salmonella* cell in which a gene encoding a heterologous antigen is inserted into a Ssp-encoding gene is also included in the invention.

30 Also within the invention is a substantially pure StpA polypeptide and a method of dephosphorylating a protein which includes the steps of contacting the protein, e.g., a protein at least one tyrosine of which is phosphorylated, with a StpA polypeptide or an active 35 fragment thereof. An active fragment of StpA is defined

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as a *Salmonella*-derived polypeptide at least 10 amino acids in length which is capable of removing a phosphate group from a tyrosine residue.

The invention features live *Salmonella*

5 (particularly *Salmonella typhimurium*) vaccines in which one or more gene required for BME is mutated so as to reduce their activity. Among the genes which can be mutated are *SspB*, *SspC*, and *SspD*. Although *SspA* appears not to be required for BME, it may be useful to mutate this gene as 10 well (preferably in combination with mutation of one or more of the other *Ssp* genes). Any mutation of these genes which decreases function, including complete or partial deletion and one or more point mutations may be useful. In addition, function of *Ssp* gene may be 15 impaired by altering its control region.

The invention provides a *Salmonella* vaccine which does not cause transient bacteremia. In general, the invention features a bacterial cell, preferably a *Salmonella* cell, e.g., a *S. typhi*, *S. enteritidis* 20 *typhimurium*, or *S. cholerae-suis* cell, the virulence of which is attenuated by a first mutation in an *Ssp* gene. The preferred mutations are loss of function mutations. However, functions causing partial loss of function may be useful if virulence is adequately reduced. Such a 25 bacterial cell can be used as a vaccine to immunize a mammal against salmonellosis.

The *Salmonella* cell may be of any serotype, e.g., *S. typhimurium*, *S. paratyphi A*, *S. paratyphi B*, *S. paratyphi C*, *S. pylorum*, *S. dublin*, *S. heidelberg*, *S. 30 newport*, *S. minnesota*, *S. infantis*, *S. virchow*, or *S. panama*.

The first mutation may be a non-revertible null mutation in one or more of the following genes: *SspB*, *SspC*, or *SspD*. Preferably, the mutation is a deletion 35 of at least 100 nucleotides; more preferably, the

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mutation is a deletion of at least 500 nucleotides; even more preferably, the mutation is a deletion of at least 750 nucleotides. Mutations in the *prgH* gene or the *prgH* operon can be used for the same purpose.

5 In preferred embodiments loss or function (partial or complete) is due to decreased expression as a result of a change or mutation, e.g., a deletion, (preferably a non-revertible mutation) at the promoter or other regulatory element of *SspB*, *SspC*, or *SspD* (or some
10 combination thereof).

In another aspect, the invention features a vaccine including a bacterial cell which is attenuated by decrease of expression of a *Ssp* virulence gene.

The invention also features a live *Salmonella*
15 cell, or a substantially purified preparation thereof, e.g., a *S. typhi*, *S. enteriditis* *typhimurium*, or *S. cholerae-suis* cell, in which there is inserted into a virulence gene, e.g., an *Ssp* gene, a gene encoding a heterologous protein, or a regulatory element thereof.

20 In another aspect the invention includes a method of vaccinating an animal, e.g., a mammal, e.g., a human, against a disease caused by a bacterium, e.g., *Salmonella*, including administering a vaccine of the invention.

25 By "vaccine" is meant a preparation including materials that evoke a desired biological response, e.g., an immune response, in combination with a suitable carrier. The vaccine may include live organism, in which case it is usually administered orally, or killed
30 organisms or components thereof, in which case it is usually administered parenterally. The cells used for the vaccine of the invention are preferably alive and thus capable of colonizing the intestines of the inoculated animal.

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By "mutation" is meant any change (in comparison with the appropriate parental strain) in the DNA sequence of an organism. These changes can arise e.g., spontaneously, by chemical, energy e.g., X-ray, or other 5 forms of mutagenesis, by genetic engineering, or as a result of mating or other forms of exchange of genetic information. Mutations include e.g., base changes, deletions, insertions, inversions, translocations or duplications.

10 A mutation attenuates virulence if, as a result of the mutation, the level of virulence of the mutant cell is decreased in comparison with the level in a cell of the parental strain, as measured by (a) a significant (e.g., at least 50%) decrease in virulence in the mutant 15 strain compared to the parental strain, or (b) a significant (e.g., at least 50%) decrease in the amount of the polypeptide identified as the virulence factor in the mutant strain compared to the parental strain.

A non-revertible mutation, as used herein, is a 20 mutation which cannot revert by a single base pair change, e.g., deletion or insertion mutations and mutations that include more than one lesion, e.g., a mutation composed of two separate point mutations.

Heterologous protein, as used herein, is a protein 25 that in wild type, is not expressed or is expressed from a different chromosomal site, e.g., a heterologous protein is one encoded by a gene that has been inserted into a second gene.

A substantially purified preparation of a 30 bacterial cell is a preparation of cells wherein contaminating cells without the desired mutant genotype constitute less than 10%, preferably less than 1%, and more preferably less than 0.1% of the total number of cells in the preparation.

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A substantially pure DNA, as used herein, refers to a nucleic acid sequence, segment, or fragment, which has been purified from the sequences which flank it in a naturally occurring state, e.g., a DNA which has been 5 removed from the sequences which are normally adjacent to the fragment, e.g., the sequences adjacent to the fragment in the genome in which it naturally occurs. The term also applies to DNA which has been substantially purified from other components which naturally accompany 10 the DNA, e.g., DNA which has been purified from proteins which naturally accompany it in a cell.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments and from the claims.

15 By "polypeptide" is meant any chain of amino acids, regardless of length or post-translational modification (e.g., glycosylation or phosphorylation).

By "substantially identical" is meant a polypeptide or nucleic acid exhibiting at least 50%, 20 preferably 85%, more preferably 90%, and most preferably 95% sequence identity to a reference amino acid or nucleic acid sequence. For polypeptides, the length of comparison sequences will generally be at least 10 amino acids, preferably at least 20 amino acids, more 25 preferably at least 25 amino acids, and most preferably 35 amino acids. For nucleic acids, the length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 30 100 nucleotides.

Sequence identity is typically measured using sequence analysis software (e.g., Sequence analysis software package of the genetics computer group, university of Wisconsin biotechnology center, 1710 35 university avenue, Madison, WI 53705). Such software

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matches similar sequences by assigning degrees of homology to various substitutions, deletions, substitutions, and other modifications. Conservative substitutions typically include substitutions within the 5 following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

By a "substantially pure polypeptide" is meant a 10 Ssp polypeptide which has been separated from components which naturally accompany it. Typically, the polypeptide is substantially pure when it is at least 60% Ssp by weight. Preferably, the preparation is at least 75%, more preferably at least 90%, and most preferably at 15 least 99%, by weight, Ssp polypeptide. A substantially pure Ssp polypeptide may be obtained, for example, by extraction from a natural source (e.g., *Salmonella* bacterium); by expression of a recombinant nucleic acid encoding a Ssp polypeptide; or by chemically synthesizing 20 the protein. Purity can be measured by any appropriate method, e.g., using column chromatography, polyacrylamide gel electrophoresis, or by HPLC analysis.

A protein is substantially free of naturally associated components when it is separated from those 25 contaminants which accompany it in its natural state. Thus, a protein which is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will be substantially free from its naturally associated components.

30 Accordingly, substantially pure polypeptides include those derived from one type of prokaryotic organism, e.g., *S. typhimurium*, but synthesized in *E. coli* or another prokaryotic organism.

By "substantially pure DNA" is meant DNA that is 35 free of the genes which, in the naturally-occurring

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genome of the organism from which the DNA of the invention is derived, flank the gene. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector; into an autonomously 5 replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote; or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a 10 recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence, e.g., a hybrid gene encoding a chimeric antigen.

Other features and advantages of the invention will be apparent from the following description of the 15 preferred embodiments thereof, and from the claims.

Detailed Description

Fig. 1 is a diagram of the a genetic map of the 59-60 min region of the *S. typhimurium* chromosome and partial physical map of the restriction endonuclease 20 sites of the *prgH* chromosomal region within the *hil* locus and related plasmids. The horizontal arrows indicate the direction of transcription of the *orfl*, *prgHIJK*, and *org* genes and of the neomycin promoter of the Tn5B50 insertions within the *hil* locus. The vertical arrows 25 indicate and the location of the predicted start of transcription of the *prgHIJK* operon (small arrow) and the location of the two Tn5B50 insertions that define the *hil* locus (large arrows). The open triangle indicates the location of the *prgH1::TnphoA* insertion. Restriction 30 endonuclease sites are as follows: B, *Bam*HI; E, *Eco*RI; H, *Hind*III; S, *Sac*I; Ss, *Ssp*I; V, *Eco*RV; X, *Xho*I.

Fig. 2 is a photograph of a Northern blot assay in which the *prgHIJK* and *org* transcripts are identified. Blot hybridization of a *prgH* (A), *prgI-J* (B) *prgK* (C), 35 *org* (D), and *pagC* (E) DNA probe to RNA purified from

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wild-type (WT) and phoP constitutive (P^C) *S. typhimurium* strains were grown aerobically to 0.5 optical density units. The bars indicate the RNA markers and are 9488, 6255, 3911, 2800, 1898, and 872 nucleotides (NT) in size 5 from top to bottom.

Fig. 3 is a photograph of a primer extension analysis of RNA isolated from wild-type and PhoP^C *S. typhimurium* strains by using an oligonucleotide primer IB08 corresponding to nucleotides 1217 to 1199 of the 10 *prgH* sequence. Lanes labeled "AGCT" represent dideoxy DNA sequencing reactions. The lane labeled "wt" represents the products of a primer extension reaction initiated with primer IB08 and wild-type RNA as a template, and the lane labeled "P^C" represents the 15 products of a primer extension reaction initiated with the same primer and PhoP^C RNA as a template. Reverse transcription of wild-type RNA with primer IB08 resulted in an approximately 270-nucleotide product corresponding to a predicted transcriptional start at nucleotide 949 of 20 the *prgH* sequence. Abbreviations: wt, wild type strain 14028s; P^C, PhoP^C strain CS022.

Fig. 4A is a diagram showing the similarity and alignment of *prgI*, *mxiiH*, and *yscF* predicted gene products.

25 Fig. 4B is a diagram showing the similarity and alignment of *prgJ* and *mxiiI* predicted gene products.

Fig. 4C is a diagram showing the similarity and alignment of *prgK*, *mxiiJ*, and *yscJ* predicted gene products. For Figs. 4A-4C, residues conserved among each 30 of the predicted gene products are indicated with a plus (+); residues conserved among the *prgI* and either the *mxiiH* or *yscF* predicted gene products and between the *prgK* and either the *mxiiJ* or *yscJ* predicted gene products are indicated with an asterisk (*). The location of the 35 lipoprotein processing sites (Leu-Xaa-Gly-Cys) of the

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prgK, *mxJ*, and *yscJ* predicted gene products are indicated by underlining. Predicted protein sequences were compared using the GCG BLAST network service and ALIGN program (Feng et al., *J. Mol. Evol.* 35:351-360, 5 1987; Higgins et al., *CABIOS* 5:151-153, 1989).

Fig. 5 is a photograph of a SDS-PAGE gel. *Salmonella* proteins found in the culture supernatant of stationary-phase *S. typhimurium* 14028s were compared to proteins isolated from lysed whole cells or cellular 10 fractions (membranes or intracellular soluble proteins). TCA precipitable material from 2 ml of supernatant from cultures of $OD_{600} = 2.2$ was used. The whole cell, membrane, and soluble lanes contained material from 0.10 ml, 0.35 ml, and 0.15 ml of cells, respectively. 15 Proteins were fractionated in a 12% polyacrylamide gel by SDS-PAGE and stained with Coomassie Brilliant Blue R-250. The molecular masses of protein standards are indicated on the side of the gel as kDa.

Fig. 6 is a photograph of a SDS-PAGE gel showing a 20 comparison of culture supernatant proteins from *S. typhimurium* 14028s and culture supernatants from mutants which are defective in eucaryotic signaling. TCA precipitable material from 2 ml of bacterial culture supernatant was isolated at different times following 25 inoculation: mid-log, $OD_{600} = 0.6$; late-log / early-stationary, $OD_{600} = 1.1$; stationary, $OD_{600} = 2.2$. Proteins were fractionated in a 12% polyacrylamide gel by SDS-PAGE and stained with Coomassie Brilliant Blue R-250. The molecular masses of protein standards are indicated 30 on the side of the gel as kDa. wt, wild type (14028s); *p^c*, *PhoP^c* (CS022); *P⁻*, *PhoP⁻* (CS015); Δ *hil* (CS451), deleted for the *hil* locus.

Fig. 7 is a photograph of a SDS-PAGE gel showing an analysis of *prgH*::TnphoA and complementation of the 35 insertion mutation by pWKSH5. TCA precipitable material

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from 2 ml of supernatant from stationary phase cultures was fractionated in a 10% polyacrylamide gel by SDS-PAGE. Protein was stained with Coomassie Brilliant Blue R-250. The molecular masses of protein standards are indicated 5 on the side of the gel as kDa. wt, wild-type (14028s); IB040, *prgH1::TnphoA*; IB043, *prgH1::TnphoA* with plasmid pWKSH5 containing a 5.1 kb insert of *S. typhimurium* DNA including *prgHIJK*. Supernatant protein bands complemented by pWKSH5 are indicated by arrows (87 kDa 10 and 65 kDa) and a bracket (three bands in the 35-40 kDa range).

Fig. 8 is a photograph of a SDS-PAGE gel showing *Salmonella* secreted proteins (Ssp) concentrated from supernatants of different strains. Each lane contains 15 Ssp collected from 2 ml of culture supernatant. Lanes 1: wild-type *S. typhimurium* SL1344; 2: EE638 (*lacZY11-6*); 3: EE633 (*lacZY4*); 4: VB122 (*hilA::kan-112*); 5: EE637 (*invF::lacZY11-5*); 6: IB040 (*prgH1::TnphoA*) St: molecular weight standard. Sizes of protein bands are given in 20 kDa. * marks a protein band which was variably present in different preparations of Ssp from the same strains.

Fig. 9 is a diagram showing the chromosomal organization of the *sspBCDA* genes and phenotypes of mutants *sspC::lacZY4* (EE633) and *sspA::lacZY11-6* (EE638). 25 The chromosomal location of *ssp* with respect to *spaT* and *prgH* is shown. An asterisk (*) indicates partially sequenced genes. Restriction sites in parentheses have only been mapped in the left region of the 11 kb *EcoRI* fragment. Abbreviations of restriction sites are: E: 30 *EcoRI*, B: *BamHI*, P: *PvuII*, N: *NcoI*. Invasion of epithelial cells by different *S. typhimurium* strains is given as the percentage of the bacterial inoculum surviving gentamicin treatment. Values represent means and standard errors of the means of three independent 35 experiments, each performed in triplicate. Presence or

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absence of *Salmonella* secreted proteins SspA, SspC and SspD in culture supernatants of different strains is indicated by + or -, respectively. The molecular weights in kDa of these Ssp are shown in parentheses.

5 Fig. 10 is a diagram showing a complementation analysis of EE638. Complementing fragments of chromosomal DNA in a low-copy plasmid are shown according to the chromosomal map. Designations of the plasmids are given in brackets on the left. The positions of the lac 10 promoter (P_{lac}) are indicated. A indicates a deletion.

Fig. 11 is a photograph of an immunoblot analysis of various strains for expression and secretion of Ssp87. Total cellular proteins from bacteria collected from 0.2 ml of cultures were loaded in lanes designated "C", 15 supernatant proteins from 0.2 ml bacterial culture supernatants were loaded in lanes designated "S". 1: wild type *S. typhimurium*; 2: CS022 ($PhoP^C$); 3: IB040 ($prgH1::TnphoA$); 4: CS451 ($\Delta hil::Tn5-428$); 5: EE638 ($sspC::lacZY11-6$); 6: EE633 ($sspA::lacZY4$).

20 Fig. 12 is a diagram showing a comparison of the deduced partial amino acid sequence of SspB with the *S. flexneri* homologue IpAB. Bars indicate identical residues, dots indicate gaps introduced in order to maximize similarity according to the GAP program of the 25 GCG package.

Fig. 13 is a diagram showing a comparison of the deduced amino acid sequences of SspC with the *S. flexneri* homologues IpAC. Bars indicate identical residues, dots indicate gaps introduced in order to maximize similarity 30 according to the GAP program of the GCG package.

Fig. 14 is a diagram showing a comparison of the deduced amino acid sequences of SspD with the *S. flexneri* homologues IpAD. Bars indicate identical residues, dots indicate gaps introduced in order to maximize similarity 35 according to the GAP program of the GCG package.

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Fig. 15 is a diagram of the amino-terminal sequence derived from the 5'-region of *sspA*. Amino acids determined by amino-terminal sequencing of *SspC* and *SspA* are underlined.

5 Fig. 16 is a photograph of a SDS-PAGE gel showing total soluble *Ssp* collected from 2 ml of culture supernatants of wild type *S. typhimurium* SL1344 and EE638 (*sspC::lacZY11-6*) transformed with various plasmids. Lanes 1: SL1344 [pWSK29]; 2: EE638 [pWSK29]; 3: EE638
10 [pCH004 (*sspC*)]; 4: EE638 [pCH005 (*sspCD*)]; 5: EE638 [pCH006 (*sspD*)]; 6: EE638 [pCH002 (*sspCDA*)]; 7: SL1344 [pCH002 (*sspCDA*)]. Lanes 8 and 9 contain soluble *Ssp* from SL1344 [pWSK29] and EE638 [pWSK29], respectively. The sizes of the protein bands are given in kDa. An
15 asterisk (*) indicates a protein band which was variably present in different preparations of *Ssp* from the same strains.

Fig. 17 is a photograph of an SDS-PAGE gel showing insoluble *Ssp* precipitates collected from 2 ml of culture
20 supernatants of wild type *S. typhimurium* SL1344 and EE638 (*sspC::lacZY11-6*) transformed with various plasmids. Lanes 1: SL1344 [pWSK29]; 2: EE638 [pWSK29]; 3: EE638 [pCH004 (*sspC*)]; 4: EE638 [pCH005 (*sspCD*)]; 5: EE638 [pCH006 (*sspD*)]; 6: EE638 [pCH002 (*sspCDA*)]; 7: SL1344
25 [pCH002 (*sspCDA*)]. Lanes 8 and 9 contain soluble *Ssp* from SL1344 [pWSK29] and EE638 [pWSK29], respectively. The sizes of the protein bands are given in kDa. An asterisk (*) indicates a protein band which was variably present in different preparations of *Ssp* from the same
30 strains.

Fig. 18 is a diagram showing the genetic organization of the invasion gene clusters from *S. typhimurium* and *S. flexneri*. The relative positions of each gene are indicated and the directions of gene
35 transcription are indicated by arrows. Arrows are not

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drawn to scale. Gene clusters conserved in sequence and gene order are indicated by stippling (*inv-spa/mxi-spa*), crosshatching (*prglJK/mxiHI*]), and dark arrows (*ssp/ipa*). Genes with no homologues within the respective regions 5 are shown as open arrows.

Fig. 19 is a depiction of the nucleic acid sequence of *SspB* (missing part of the 5' end) (SEQ ID NO: 1).

Fig. 20 is a depiction of the nucleic acid 10 sequence of *SspC* (SEQ ID NO: 2).

Fig. 21 is a depiction of the nucleic acid sequence of *SspD* (SEQ ID NO: 3).

Fig. 22 is a depiction of the nucleic acid sequence of *SspB* (missing part of the 3' end) (SEQ ID NO: 15 4) and the predicted amino acid sequence *SspB* (partial c-terminal) (SEQ ID NO: 5).

Fig. 23 is a depiction of the predicted amino acid sequences of *SspC* (SEQ ID NO: 6), *SspD* (SEQ ID NO: 7), and *SspA* (partial amino terminal) (SEQ ID NO: 8).

20 Fig. 24 is a depiction of the nucleic acid sequences of *iagB* (SEQ ID NO: 9) and *stpA* (SEQ ID NO: 10).

Fig. 25 is a depiction of the predicted amino acid sequences of *iagB* (SEQ ID NO: 11) and *stpA* (SEQ ID NO: 25 12).

Fig. 26 is a depiction of the nucleic acid sequence of *prgH* (SEQ ID NO: 13).

Fig. 27 is a depiction of the predicted amino acid sequences of *prgB* (SEQ ID NO: 14).

30 Fig. 28 is a depiction of the nucleic acid sequence of *SspBCDA* (truncated at 3' and 5' ends) (SEQ ID NO: 15).

Fig. 29 is a depiction of the nucleic acid 35 sequence of *prgH* and 5' and 3' flanking sequences (SEQ ID NO: 16).

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Ssp Proteins and Genes

The *Salmonella* secreted proteins (Ssp) of the invention have a variety of uses. For example, they can be used as diagnostic reagents, therapeutic agents, and 5 research products. The genes encoding Ssp also have a variety of uses. For example, they can be used as diagnostic reagents. They can also be used to create vaccines including live attenuated vaccines.

Because *Salmonella* infection is a significant 10 health problem and because Ssp proteins are soluble proteins that are found on the surface of *Salmonella*, various Ssp, DNA encoding various Ssp, and antibodies directed against various Ssp are useful in diagnostic assays. Because Ssp are required for optimal virulence, 15 DNA encoding a mutant Ssp having decreased function can be used to create strains of *Salmonella* with reduced virulence. Such strains are useful as live vaccines.

An Ssp (or a portion thereof which can gain entry into the cytoplasm) can be used to translocate a second 20 molecule, e.g., a polypeptide, into the cytoplasm of a cell. This approach can be useful for the induction or priming of cytotoxic lymphocytes (CTL) directed against the second molecule. An Ssp (or a portion thereof capable of translocating an attached second molecule) can 25 be used to introduce a second molecule into the cell cytoplasm for the purpose of drug delivery. Often the second molecule is a polypeptide which is covalently linked to an Ssp (or a portion thereof), e.g., by a peptide bond. Such molecules can be readily produced 30 first preparing a chimeric gene encoding the Ssp (or portion thereof) and the second molecule as a single polypeptide chain. This gene can be used to prepare the fusion protein for administration to a patient. Alternatively, the chimeric gene can be introduced into a

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strain of *Salmonella* which can then be used as either a live vaccine or drug delivery system.

Ssp as Diagnostic Reagents

An Ssp can be used as a diagnostic tool for the 5 detection of *Salmonella* infection in a patient or to evaluate status of an immune response to *Salmonella*. For example, one or more Ssp can be used as an antigen in an ELISA assay to detect the presence of *Salmonella*-specific antibodies in a bodily fluid, e.g., blood or plasma, 10 obtained from an infected patient or an individual suspected of being infected with *Salmonella*. Ssp can also be used to test immune cell activation, e.g., T or B cell proliferation or cytokine production, in a sample of patient-derived cells, e.g., peripheral blood mononuclear 15 cells, to detect the presence of a cellular immune response to *Salmonella*.

Polynucleic acids (e.g., primers and probes) encoding all or part of an Ssp can be used in hybridization assays to detect the presence *Salmonella* 20 infection, e.g., using a PCR assay or other probe or primer based assay designed to detect particular DNA sequences.

Antibodies capable of selectively binding a particular Ssp can be used to detect the presence of 25 *Salmonella* in a biological sample. Such antibodies can be produced using standard methods.

Therapeutic Applications of Ssp Fusion Proteins

Fusion proteins comprising all or part of an Ssp and a second protein or polypeptide are useful for a 30 variety of therapeutic applications such as vaccines (e.g., recombinant *Salmonella* vaccines or vaccines against heterologous pathogens), cell targeting agents for delivery of drugs (e.g., cytotoxic agents), and adjuvants, (e.g., to boost an immune response to a co- 35 administered antigen).

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To produce a recombinant *Salmonella* vaccine, a gene encoding an Ssp fusion protein can be introduced into a *Salmonella* vaccine. Because Ssp are involved in bacterial mediated endocytosis, the Ssp fusion protein 5 will cause the second polypeptide or protein to be internalized by epithelial cells (or other cells to which the Ssp binds) of the individual to which the vaccine is administered. This internalization can trigger a Type I MHC-mediated response to the second protein or 10 polypeptide. The induction of this response will lead to the induction of CTL (or the priming of CTL) specific for the second protein or polypeptide. The induction or priming of antigen-specific CTL can provide therapeutic or prophylactic benefits.

15 Purified fusion proteins can be used as recombinant vaccines. Proteins fused to Ssp are specifically targeted to epithelial cells or other cell types to which the Ssp bind; the fusion proteins are then internalized by the targeted cells. Thus, Ssp fusion 20 proteins are useful to generate an immune response to the antigen to which the Ssp is linked or to deliver a therapeutic compound, e.g., a toxin for the treatment of cancer or autoimmune diseases in which the killing of specific cells, i.e., the cells to which a Ssp binds, is 25 desired. Delivery of a toxin linked to a SspC or SspD polypeptide is especially useful in cancer therapy because man types of cancers are of epithelial cell origin.

20 Ssp fusion proteins which contain all or part of a Ssp linked to a heterologous protein can be made using methods known in the art. Two or more polypeptides may be linked together via a covalent or non-covalent bond, or both. Non-covalent interactions can be ionic, hydrophobic, or hydrophilic.

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A covalent linkage may take the form of a disulfide bond. For example, the DNA encoding one of the polypeptides can be engineered to contain a unique cysteine codon. The second polypeptide can be 5 derivatized with a sulfhydryl group reactive with the cysteine of the first component. Alternatively, a sulfhydryl group, either by itself or as part of a cysteine residue, can be introduced using solid phase polypeptide techniques.

10 A number of other covalent crosslinking agents, e.g., photoreactive crosslinkers, water-soluble crosslinkers, which are commercially available may be used to join a heterologous polypeptide to a Ssp to create a fusion protein. If the fusion protein is 15 produced by expression of fused genes, a peptide bond serves as the link between the components of the fusion protein. Such fusion proteins are produced by expression of a chimeric gene in which sequences encoding all or part of an Ssp are in frame with sequences encoding the 20 second protein or polypeptide. In some circumstances it may be useful to include a linker polypeptide between the Ssp and second protein of polypeptide.

Internalization of the fusion protein may not require the presence of a complete Ssp protein. A 25 internalization-competent portion of an Ssp will be adequate in many circumstances. Whether a particular portion of a selected Ssp is sufficient for internalization can be tested as follows. The selected portion of an Ssp is fused to a calmodulin-dependent 30 adenylate cyclase. If this test fusion protein is internalized, it will be exposed to calmodulin and the cyclase will be activated. The presence of adenylate cyclase activity can then be used as a measure of internalization. This general approach is described by 35 Sorg et al. (*Molecular Microbiol.* 14:583-94, 1994).

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Ssp are virulence factors that alter the ability of bacteria to be internalized by specific populations of host cells and to induce an immune response. *Salmonella* with mutations in genes encoding Ssp are useful in the 5 manufacture of live *Salmonella* vaccines with altered cell tropism.

Deletion or overexpression of Ssp in *Salmonella* can be used to target strains or fusion proteins to various mammalian cell types. Invasion of epithelial 10 cells or macrophages can be selected depending on the Ssp mutated. For example, use of *Salmonella* as an antigen or drug delivery vehicle can be optimized by deleting part or all of a gene encoding a Ssp involved in bacterial mediated endocytosis (or mutating such a gene to impair 15 Ssp function), thereby minimizing the ability of *Salmonella* to invade epithelial cells (and therefor maximizing antigen delivery to antigen presenting cells such as macrophages). In this manner, strains with mutated Ssp genes can be used to modulate the host immune 20 system. Deletion of Ssp genes in *Salmonella* can also be used to alter the ability of *Salmonella* to stimulate IL-8 secretion by epithelial cells.

Fusions of antigens to Ssp genes can be used to facilitate an immune response to the linked antigens for 25 the purpose of generating an antigen-specific cytotoxic T cell response in a patient. For example, Ssp fusions to viral antigens are useful as therapeutic vaccines for diseases such as AIDS and *Herpes genitalis* in which the generation of a cytotoxic T cell (CTL) response is 30 desired. Delivery of antigens in this manner favors the generation of an antigen-specific CTL response because the Ssp portion of Ssp fusion protein mediates translocation of the fusion protein across eucaryotic cell membranes into the intracellular compartments in the 35 cytoplasm of cells which participate class I MHC-mediated

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antigen processing and presentation, i.e., the generation of class I MHC-restricted antigen-specific CTLs.

Fusion proteins which include all or part of a Ssp linked to a cytotoxic molecule can be used to target a 5 cytotoxic molecule to a specific cell type, e.g., an epithelial cell-derived cancer cell, which would then be killed by the cytotoxic agent. Cytotoxic fusion proteins can be synthetically or recombinantly produced and administered directly to a patient. Alternatively, live 10 *Salmonella* expressing a cytotoxic Ssp fusion protein can be administered and allowed to produce and secrete the fusion protein *in vivo*.

Ssp are also useful as adjuvants to boost the immunogenicity of antigens with which they are delivered 15 or to which they are chemically or recombinantly linked. Ssp that have enzymatic effects, e.g., phosphatase activity, on certain types of eucaryotic cells can be used to promote specific types of immune responses such as TH2 or TH1 T cell responses. Since these proteins are 20 secreted and are likely taken up in the cytoplasm of eucaryotic cells, gene fusions to these proteins are likely to be more immunogenic and more efficient in inducing the development of an immune response, particularly a class I MHC-restricted CTL response.

25 Various oral and parenteral delivery systems are known in the art and can be used to deliver the Ssp polypeptides and/or chimeric antigens of the invention, such as encapsulation in liposomes, or controlled release devices. The compositions of the invention can be 30 formulated in a pharmaceutical excipient in the range of approximately 10 µg/kg and 10 mg/kg body weight..

The compositions and methods of the invention provide the tools with which to construct better vaccines against *Salmonella* infection and for the prevention and 35 treatment of other diseases, e.g., cancer and AIDS, by

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using *Salmonella* secreted proteins as carriers of heterologous antigens, e.g., tumor antigens or viral antigens, either as purified components or as hybrid proteins produced in live *Salmonella* vaccine strains.

5 Ssp and Attenuated Bacterial Strains

Deletion or mutation of one or more Ssp genes can be used to attenuate vaccine strains. For instance deletion of Ssp genes leads to lack of neutrophil transmigration across epithelial cell

10 monolayers (a model system that correlates well with the ability of certain strains to cause gastroenteritis).

Vaccine strains are usually administered at doses of 1×10^5 to 1×10^{10} cfu/single oral dose. Those skilled in the art can determine the correct dosage using 15 standard techniques.

Research products

Ssp with enzymatic activity, e.g., *Salmonella* tyrosine phosphatase (stpA), can be used as reagents for protein modification. StpA catalyzes the release of 20 phosphate groups from tyrosine residues in proteins, and thus, is especially useful in the field of signal transduction. Since a number of eucaryotic and procaryotic signal transduction proteins are regulated by the phosphorylation and dephosphorylation of tyrosine 25 residues, stp can be used to deactivate or activate these proteins, thereby altering intracellular signal transduction. Thus, Stp can be used as a research tool to study and evaluate phosphorylation-regulated signal transduction pathways.

30 Modification of Ssp and Ssp Variants

When an Ssp is being used to translocate a second molecule into a eukaryotic cell, it may be useful to increase expression of the Ssp (or Ssp fusion protein) so that BME is increased. Increased expression of *sspc*, 35 *sspD* and other *ssp* genes may be accomplished using

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methods known in the art, e.g., by introducing multiple copies of the gene(s) into the bacterial cell or cloning the Ssp-encoding DNA under the control of a strong promoter.

5 Under other circumstances it may be desirable to increase uptake of a bacterial strain, e.g., a *Salmonella* strain, by a macrophage in a mammal by impairing the normal invasion mechanism of the strain. This can be accomplished by decreasing expression of the DNA encoding 10 the SspC and/or SspD (and thereby decreasing secretion of Ssp and/or SspD polypeptides) and administering the cell to the mammal. Ssp expression may be reduced using methods known in the art, e.g., insertion of a transposon (Tn) into the gene, deletion of some or all of the gene, 15 mutating a gene upon which SspC and/or SspD expression depends, e.g., *prgH*, e.g., a deletion or Tn insertion in the *prgHIJK* operon. Instead of decreasing the expression of *sspC* and/or *sspD*, the method may include the step of impairing the function of one or both of the gene 20 products, e.g., by Tn insertion, deletion mutagenesis, or by impairing the secretory pathway by which the gene products are secreted such that the gene products are produced but not effectively transported to the extracellular environment.

25 Example 1: PhoP/PhoQ Transcriptional Repression of *S. typhimurium* Invasion Genes: Evidence for a Role in Protein Secretion

The PhoP-repressed *prgH* locus of *S. typhimurium* may be important for signaling epithelial cells to 30 endocytose *S. typhimurium*. The following series of experiments demonstrate that the *prgH* locus is an operon of four genes encoding polypeptides of 392 amino acids (*prgH*), 80 amino acids (*prgI*), 101 amino acids (*prgJ*), and 252 amino acids (*prgK*). These experiments also

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demonstrate that expression of the 2.6-kb *prgHIJK* transcript is reduced when *PhoP/PhoQ* is activated, suggesting that *PhoP/PhoQ* regulates *prgHIJK* by transcriptional repression. Further, analysis of the 5 culture supernatants from wild-type *S. typhimurium* revealed the presence of at least 25 polypeptides larger than 14 kDa. Additional experiments demonstrated that *prgH1::TnphoA*, *phoP* constitutive (*PhoP^C*), and *hil* deletion mutants have significantly defective supernatant 10 protein profiles. A further set of experiments described below demonstrate that both the invasion and supernatant protein profile defects of the *prgH1::TnphoA* mutant can be complemented by a 5.1 kb plasmid that included *prgHIJK*. Taken together these results suggest that 15 *PhoP/PhoQ* regulates extracellular transport of proteins by transcriptional repression of secretion determinants and that secreted proteins are likely involved in signaling epithelial cells to endocytose bacteria.

The following reagents and procedures were used to 20 evaluate the *prgH* locus.

Bacterial Strains, Growth and Conditions

S. typhimurium strain ATCC 14028s (American Type Culture Collection, Bethesda, MD) is a virulent wild-type parent strain from which all other *Salmonella* strains 25 described in Example 1 were derived. Bacterial strains and plasmids are described in Table 1. Luria-Bertani broth (LB) was used as rich bacterial growth medium. Antibiotics were added to LB broth or agar in the following concentrations: ampicillin, 25 µg/ml; 30 chloramphenicol, 50 µg/ml; kanamycin, 45 µg/ml.

DNA sequencing and analysis

Double-strand templates were sequenced by the dideoxy-chain termination method known in the art as modified for use with Sequenase™ (US Biochemicals, Corp.) 35 and [α -³⁵S]dATP. Computer analysis of the DNA sequence

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was accomplished with the GENEPRO (Riverside Scientific, Riverside, CA) and Wisconsin package (GCG, version 7) programs. The nucleotide sequence of the *prgHIJK* locus has been deposited in GeneBank under accession number 5 U21676.

RNA extraction, RNA blot analyses, and primer extension analyses

RNA was isolated from mid-log phase cultures (OD₆₀₀ = 0.5) of aerobically-grown (with shaking) and 10 microaerophically-grown (without shaking) *Salmonella* strains using a standard hot phenol procedure (Pulkkinen et al., *J. Bacteriol.* 173:86-93, 1993). For RNA blots, 20 µg of RNA was diluted in H₂O and incubated for 15 minutes at 55°C in 50% formamide, 17.5% formaldehyde in 1 15 × Northern buffer (0.36 M Na₂HPO₄·7H₂O, 0.04 M NaH₂PO₄·H₂O). Samples were run on 1% agarose gels containing 6% formaldehyde and 1 × Northern buffer and were transferred to Gene Screen Plus membranes (NEN/Dupont). RNA was crosslinked to the membrane using 20 a Stratalinker™ UV crosslinker (Stratagene, La Jolla, CA). Membranes were hybridized and washed according to the manufacturer's protocol.

The DNA probes for RNA-DNA and DNA-DNA blot hybridization were obtained from recombinant plasmid DNA 25 by restriction endonuclease digestion or by polymerase chain reaction (PCR) using the GeneAmp™ PCR kit (Perkin-Elmer/Cetus). The following DNA probes were synthesized: a 841-bp *prgH* probe from the oligonucleotide primers IB07 (5'-CCAGGTGGATACGGA-3'; SEQ ID NO: 17; 30 nucleotides 1198 to 1212) and IB19 (5'-TAGCGTCCTCCCCATGTGCG-3'; SEQ ID NO: 18; nucleotides 2039 to 2021); a 433-bp *prgI-prgJ* probe from the primers IB26 (5'-CCGGCGCTACTGGCGGCG-3'; SEQ ID NO: 19), nucleotides 2304 to 2321) and DP04 35 (5'AGCGTTTCAACAGCCCCG-3'; SEQ ID NO: 20), nucleotides

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2737 to 2719); a 341-bp *prgK* probe from primers DP03
(5'-CGGGGCTGTTGAAACGC-3'; SEQ ID NO: 21), nucleotides
2720 to 2736) and DP08 (5'-AACCTGGCCTTTCAG-3'; SEQ ID
NO: 22), nucleotides 3060 to 3045); a 724-bp *org* probe
5 from primers DP15 (5'-GGCAGGGAGCCTTGCTTGG-3'; SEQ ID NO:
23), nucleotides 3774 to 3792) and DP17
(5'-GTGCCTGGCCAGTTCTCCA-3'; SEQ ID NO: 24); and a 608-bp
pagC probe from a *Psi* and *Stu*I restriction-endonuclease
digest of pWPL4 that contains the wild-type *pagC* gene.
10 DNA probes were radiolabelled using a standard method of
random priming with [α -³²P]dCTP.

For primer extension analyses, oligonucleotide
primers (0.2 picomoles) were end-labelled with [γ -³²P]dATP
(NEN/Dupont), annealed to *S. typhimurium* RNA (20 μ g) and
15 extended with reverse transcriptase (Gibco BRL, St.
Louis, MO). Reactions were electrophoresed in 6%
polyacrylamide, 8 M urea gels adjacent to sequencing
reactions initiated with primers used for cDNA synthesis.
DNA blot hybridization analysis

20 Chromosomal DNA was isolated, restriction
endonuclease digested, size fractionated in agarose gels,
and transferred to GeneScreen Plus membranes
(NEN/Dupont). For dot blot hybridization experiments,
high stringency hybridization was performed according to
25 standard methods at 65°C using radiolabelled probes.

Protein isolation and analysis

Bacteria were grown in LB, with shaking at 37°C.
Bacterial cultures were chilled to 4°C and centrifuged at
154,000 \times g for 1.7 hours. The supernatant was carefully
30 removed and trichloroacetic acid (TCA) was added to a
final concentration of 10%. The precipitates were
collected by centrifugation at 69,000 \times g for 1 hour,
rinsed with cold acetone, dried and stored at 4°C. The
bacterial cell pellet was fractionated to obtain
35 periplasmic, cytoplasmic, and membrane fractions.

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Samples were analyzed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) on a 10-12% polyacrylamide (0.1 M Tris pH 8.45, 0.1% SDS) gel using a standard Tris-glycine buffer system or 5 standard Tris-tricine buffer system. TCA precipitates were mixed with sample buffer (250 mM Tris pH 6.8, 2% SDS, 0.0025% bromophenol blue, 5.0% β -mercaptoethanol, 10% glycerol) and heated to 100°C for 5 minutes. Proteins were visualized by staining with Coomassie 10 Brilliant Blue R-250.

Enzyme assays

Presence of the marker enzymes, alkaline phosphatase (periplasm) and β -galactosidase (cytoplasm) were used to assess fraction purity. A plasmid, pPOS3, 15 containing an arabinose-inducible *phoA* gene, was inserted into wild-type strain 14028s by transformation and moved into other strains using P22 bacteriophage-mediated transduction. Addition of arabinose (0.02%) to the culture medium induced transcription of the *phoA* gene. 20 Determination of alkaline phosphatase activity of strains containing pPOS3 was performed using the substrate p-Nitrophenyl phosphate according to standard methods. The results were expressed in standard units for β -galactosidase (Miller, J.H., 1972, *Experiments in 25 Molecular Genetics*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., pp. 352-355). β -galactosidase was produced from a strain with a *mudJ*-generated gene fusion of *msg* and *lacZ*. The gene, *msg*, is constitutively expressed and not PhoP regulated. β -galactosidase 30 activity of strains carrying *msg::MudJ* was measured using routine methods (Miller et al., *supra*).

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Table 1. Bacterial strains, plasmids and relevant properties

	<u>S. typhimurium</u>	<u>Relevant genotype</u>
	ATCC 14028s	Wild Type
5	CS002	<i>pho-24</i>
	CS019	<i>phoN2zxx::6251Tn10d-Cm</i>
	IB040	CS019 with <i>prgH1::TnphoA</i>
	IB043	IB040 with pWKSH5
	CS015	<i>phoP-102::Tn10d-Cm</i>
10	CS451	14028s derivative of EE451 with Δ hil

Escherichia coli

DH5 α F $^-\Phi 8\Phi$ lacZ Δ M15 Δ (*lacZYA-argF*) U169endA1
recA1hsdR17deoRthi-1supE44λgyrA96relA1

Plasmids

15	pIB01:	pUC19 (amp^R) containing a 10.7-kb <i>EcoRV</i> fragment with <i>prgH1::TnphoA</i> (kan^R)
	pVB3	pUC19 containing a 5.9-kb <i>HindIII-EcoRI</i> fragment of the <i>prgH</i> locus
20	pWKSH5	pWKS30 (amp^R) containing a 5.1-kb <i>HindIII</i> fragment of the <i>prgH</i> locus
	pWPL4	pUC19 containing a 5.0-kb <i>EcoRV</i> fragment of the <i>pagC</i> locus
	pPOS5	pBR322 containing arabinose-inducible PhoA

Cloning and sequencing of *prgH*

25 The DNA containing the *prgH1::TnphoA* gene fusion was cloned based upon information derived from the physical map of restriction endonuclease sites surrounding the transposon insertion (Fig. 1) (Behlau et al., *J. Bacteriol.* 175:4475-4484, 1993, hereby incorporated by reference). Chromosomal DNA from strain IB040 containing the *prgH1::TnphoA* insertion was digested with the restriction endonuclease *EcoRV* and ligated into *SmaI* digested pUC19 to generate a library of recombinant plasmids. These recombinant plasmids were transformed 30 into *Escherichia coli* (*E. coli*) DH5 α . A recombinant plasmid containing a 10.7 kb *EcoRV* fragment was 35 identified by selecting for kanamycin resistance (*TnphoA*

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encoded) and was designated pIB01 (Fig. 1). DNA hybridization analysis of strain IB040 with a radiolabelled 1.5-kb *Hind*III-*Sac*I-generated DNA fragment of pIB01 resulted in hybridization to an approximately 5 10.7-kb *Eco*RV DNA fragment. This was approximately 7.7 kb (the size of *Tnpho*A) larger than the 3-kb fragment present in the wild-type strain ATCC 14028s. This probe also hybridized strongly to plasmid pVB3 that contained the 5.9 kb *Hind*III-*Eco*RI fragment of the *hil* locus (Fig. 10 1), confirming the location of the *prgH* locus within this region. This data indicated DNA containing the *prgH1::Tnpho*A insertion had been cloned.

The DNA sequence of the 4,034-bp *Hind*III-*Ssp*I fragment (within which the *Tnpho*A insertion in *prgH* was 15 localized) was determined by sequencing plasmid pIB01 containing the cloned *prgH1::Tnpho*A allele. This sequence was confirmed by DNA sequencing of pWKSH5 containing the wild-type *prgH* allele (Fig. 1). Information from DNA sequence of the *prgH1::pho*A fusion 20 junction was used to determine the direction of transcription and correct reading frame of *prgH*. *Tnpho*A was inserted after nucleotide 1548 within an open reading frame that extended from nucleotides 981 to 2156. *prgH* was predicted to encode a 392 amino acid polypeptide with 25 a calculated M_r of 44,459 daltons and pI of 5.86. The N-terminal portion of *prgH* was found to have a stretch of nonpolar residues followed by the motif Leu-Xaa-Gly-Cys at residues 24 to 27 (corresponding to nucleotides 1050 to 1061) characteristic of the processing site of 30 bacterial lipoproteins. There was a strong hydrophobic domain (amino-acid residue 144 to 154, corresponding to nucleotides 1410 to 1433) upstream of the *Tnpho*A insertion.

Analysis of the nucleotide sequence located 35 upstream of *prgH* revealed an additional open reading

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frame from nucleotides 665 to 222, termed *orf1*, likely to be oppositely transcribed from *prgH*. The intergenic region between *orf1* and *prgH* was 216 nucleotides. *orf1* was predicted to encode a gene product of 148-amino-acid residues with a calculated M_r of 17,186. The start codon of *orf1* was preceded by a potential ribosome binding site at 7 to 11 nucleotides 5' to the predicted start of translation (5'-AAAGG-3', nucleotides 676 to 672) suggesting that this open reading frame was translated.

10 The *orf1* predicted gene product had no signal sequence nor any strong hydrophobic domains.

Identification of *prgI*, *prgJ*, and *prgK*

Analysis of the nucleotide sequence located downstream from *prgH* revealed four additional open reading frames that were predicted to be transcribed in the same direction and form an operon: (a) nucleotides 2184 to 2423; (b) nucleotides 2445 to 2747; (c) nucleotides 2747 to 3502; and (d) nucleotide 3476 to beyond the 3' *SspI* site. The first three of these four open reading frames identified were designated *prgI*, *prgJ*, and *prgK* respectively. *prgI*, *prgJ*, and *prgK* were predicted to encode gene products of 80 amino acids (M_r , 8865 daltons), 101 amino acids (M_r , 10,929 daltons), and 252 amino acids (M_r , 28,210 daltons). The predicted gene products encoded by *prgI* and *prgJ* did not contain a signal sequence or strong hydrophobic domains. The predicted gene product encoded by *prgK* contained a N-terminal hydrophobic region followed by a potential lipoprotein processing site from amino-acid residue 15 to 18 (corresponding to nucleotides 2788 to 2800). The fourth open reading frame corresponded in DNA sequence to the *S. typhimurium* oxygen-regulated gene (*org*).

prgH-K transcription is negatively regulated by *PhoP/PhoQ*

To determine whether *prgH* was negatively regulated by *PhoP/PhoQ*, RNA isolated from wild-type (ATCC 14028s)

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and *PhoP^C* (CS022) strains of *S. typhimurium* were analyzed. In numerous RNA blot analyses, the *prgH*-specific DNA probe hybridized with an approximately a 2600-nucleotide RNA from the wild-type strain (Fig. 2).

5 The size of the RNA that hybridized to the *prgH* probe was similar to that of the *prgH-K* open reading frame predicted from the DNA sequence (i.e., 2600 vs. 2522 nucleotides). In contrast, no transcript was seen when equal amounts and similar quality of RNA (as assessed by 10 methylene blue staining) isolated from the *PhoP^C* strain was probed with *prgH*-specific DNA (Fig. 3). In comparison, when the same RNA preparations were hybridized with a *pagC*-specific probe, an approximately 1100-nucleotide *pagC* transcript was highly expressed in 15 the *PhoP^C* strain (Fig. 2), consistent with the constitutive phenotype of *pag* gene expression in the *PhoP^C* mutant (Pulkkinen et al., *J. Bacteriol.* 173:86-93, 1991, hereby incorporated by reference). These results indicate that regulation of *prgH* occurs at the level of 20 transcription.

Primer extension analysis was performed to obtain information on the possible initiation site of *prgH* transcription. Based on this analysis, the start of *prgH* transcription was predicted to begin approximately 25 32 nucleotides upstream from the *prgH* translational start (Fig. 3). Several different primers were used that resulted in primer extension products of differing lengths, but all predicted that transcription initiated at this site. The predicted -10 (5'-TAATCT-3') and -35 30 (5'-TTCATC-3') regions are similar to the consensus sequences for typical *α*70 *E. coli* promoters. Similar to the results of RNA blot hybridization analysis, a primer extension product was detected only with RNA isolated from wild-type *S. typhimurium* and not with RNA isolated 35 from the *PhoP^C* strain (Fig. 3).

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The size of the RNA that hybridized to the *prgH*-specific probe suggested that *prgH-K* could form a transcriptional unit. Therefore, to determine whether *prgI-K* formed an operon that was regulated by *PhoP/PhoQ*,

5 RNA blot hybridization and primer extension analysis were performed using DNA probes and primers specific to the *prgI*, *prgJ*, and *prgK* open reading frames. Similar to the results with *prgH*, the *prgI-J-* and *prgK*-specific DNA probes hybridized with an approximately 2600-nucleotide

10 RNA isolated from wild-type *S. typhimurium* and not with RNA from the *PhoP^C* strain (Fig. 2). No primer extension products less than 350 nucleotides were detected using RNA isolated from either the wild-type or *PhoP^C* strains using *prgI*, *prgJ*, and *prgK* primers. These primers were

15 from 1662 to 2332 nucleotides downstream from the predicted start of *prgH* transcription. These findings indicated that *prgH-K* were transcribed as an operon, heretofore referred to as *prgHIJK*. Furthermore, this operon was likely to be transcribed from the *prgH*

20 promoter and was negatively regulated by *PhoP* at the level of transcription.

org is not regulated by *PhoP/PhoQ*

Although the above results suggested that the *prgHIJK* transcriptional unit did not include *org*,

25 experiments were performed to test this possibility. Blot hybridization analysis was performed with RNA isolated from wild-type *S. typhimurium* and an *org*-specific DNA probe. As shown in Fig. 2, two distinct transcripts hybridized to the *org* probe: an approximately 30 1400-nucleotide abundant RNA and a minor RNA of approximately 3800 nucleotides. The size of the smaller RNA was similar to that of the *org* open reading frame (1400 vs. 1236 nucleotides). In comparison, only the major 1400-nucleotide RNA was seen when RNA from the 35 *PhoP^C* strain was hybridized with the *org*-specific DNA

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probe, suggesting that the 3800-nucleotide RNA was PhoP repressed.

A minor RNA of approximately 3800 nucleotides also was detected in long exposure of wild-type RNA blots that 5 were hybridized with either the *prgH*, *prgI-J*, or *prgK* probes, suggesting possible cotranscription of *prgHIJK* and *org*. However, both the major (1400 nucleotide) and minor (3800 nucleotide) transcripts were detected when RNA isolated from the *prgH1::TnphoA* strain was 10 hybridized with the *org* probe, indicating that the *prgH1::TnphoA* insertion was not polar on either of the *org* transcripts. Because expression of an *org::lacZY* fusion was shown to be increased approximately fourteen fold in low-oxygen compared with high-oxygen tension, RNA 15 from wild-type and *PhoP^C* strains that were grown aerobically or microaerophically to an optical density at 260 nm of 0.5 were compared by blot hybridization with the *org*-specific DNA probe. No substantial difference was seen in the relative amounts of RNA transcripts 20 detected in wild-type or *PhoP^C* strains grown under these conditions. These data indicate that *org* did not form part of the *prgHIJK* operon and that it was not regulated by *PhoP/PhoQ*.

The *prgI*, *prgJ*, and *prgK* predicted polypeptides are 25 similar to *S. flexneri* *Mxi* and *Y. enterocolitica* *Ysc* proteins

The sequences of the five predicted polypeptides (*Prgh*, *PrgI*, *PrgJ*, *PrgK*, and *Orf1* were compared with the protein sequences translated from the GeneBank library 30 using BLAST network software. This comparison revealed similarity between the predicted products of *prgI*, *prgJ*, and *prgK* and the *MxiH*, *MxiI*, and *MxiJ* proteins of *S. flexneri*. Each of the these polypeptide sequences were similar over their entire length, with 65% (*PrgI* vs. 35 *MxiH*), 38% (*PrgJ* vs. *MxiI*), and 46% (*PrgK* vs. *MxiJ*) of

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positions occupied by identical residues (Figs. 4A-4C). The *prgI* and *prgK* predicted gene products were also similar to the *YscF* and *YscJ* proteins, respectively, of *Y. enterocolitica*, with 28% and 308 of positions occupied by identical residues. The Poisson probabilities were highly significant for each of these comparisons. No protein similar to the *prgH* or *orfl* predicted polypeptides was detected in the protein sequence library.

10 Isolation of proteins from *S. typhimurium* culture supernatants

The role of *prgHIJK* in *S. typhimurium* protein secretion was analyzed by examination of the proteins present in cell culture supernatant. Culture media of 15 wild-type bacteria was collected for protein analysis by centrifuging stationary phase cultures at 154,000 \times g for 1.7 hours. From 6-8 μ g/ml of protein was precipitated by addition of trichloroacetic acid (TCA) to overnight culture supernatants. The TCA-precipitable material in 20 ml of supernatant then was fractionated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) (Fig. 5). Approximately 25 protein bands, ranging in molecular mass from 18-87 kDa, were detected by Coomassie brilliant blue staining.

25 To rule out the possibility that the supernatant protein bands represented proteins released from lysed cells, soluble and membrane fractions of whole cells and whole cell lysates were compared with proteins from the supernatant by SDS-PAGE (Fig. 5). Many of the major 30 polypeptides in the supernatant (e.g., the polypeptide with molecular mass of 87 kDa) were not the major proteins in the other cellular fractions. Conversely, major intracellular soluble proteins and membrane proteins (e.g., the 36 kDa OmpC porin) were not detected 35 in the supernatant in this analysis. In addition,

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following centrifugation, the overnight culture media from bacteria expressing alkaline phosphatase (a periplasmic protein) and β -galactosidase (a cytoplasmic protein) always contained less than 9% and 1%, 5 respectively, of the whole-cell activity of these enzymes. Although some of the supernatant protein bands may represent degradation products of larger protein species, these data indicate that *S. typhimurium* was capable of significant protein secretion.

10 To determine the timing of release of polypeptides in to the supernatant and to test for an effect of PhoP regulon mutations on secretion, supernatants from CS015, with a null mutation in PhoP (PhoP⁻), CS022 (PhoP^C), and wild-type bacteria (ATCC 14208s) were compared. As shown 15 in Fig. 6, the quantity of protein increased for each strain when supernatant samples taken from mid-log-phase ($OD_{600} = 0.6$), late-log/early-stationary-phase ($OD_{600} = 1.1$), and stationary-phase ($OD_{600} = 2.2$) were compared. However, the pattern of major protein bands detected for 20 each strain was unchanged from mid-log to stationary phase (Fig. 6).

Altered supernatant protein profiles of mutants defective in signaling epithelial cells

At each phase of growth examined, a similar 25 pattern and quantity of protein was detected in the culture supernatants of PhoP⁻ strain CS015 and wild-type bacteria (Fig. 6). In contrast, the protein level of 2 ml of PhoP^C strain CS022 supernatant was 24% of wild type levels. At least 10 major protein bands seen in the 30 wild-type supernatant were greatly reduced or undetectable by Coomassie blue staining of the CS022 supernatant, especially those of higher molecular weight (Fig. 6). In addition, four major protein bands appeared to be increased in amount in CS022 compared with 35 wild-type supernatant (31.5 kDa, 30 kDa, 23 kDa, and 20

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kDa) (Fig. 6). Although this result could be due to degradation of higher molecular weight polypeptides, these data suggest that the *PhoP^C* mutant likely was defective in synthesis or secretion of *Ssp*.

5 The defect observed with the *PhoP^C* mutant was consistent with *prg* gene products having a role in protein secretion. Therefore, the *Ssp* of strains having transposon insertion or deletion of *prgHIJK* were compared to wild-type bacteria (ATCC 14028s) by SDS-PAGE. As 10 observed for the *PhoP^C* mutant, IB040 (*prgH1::TnphoA*) and CS451, containing a 10-kb deletion of *hil* locus (*Δhil*) DNA, each had a pronounced defect in their *Ssp* profile compared with the wild-type strain (Fig. 6 and 7). IB043 and CS451 culture supernatants contained 100% and 62%, 15 respectively, of wild-type protein levels. At least 5 and 11 major protein bands seen in the wild-type supernatant were greatly reduced or undetectable by Coomassie blue staining of the IB040 and CS451, respectively. Five protein bands [87 kDa, 65 kDa, and 20 three in the 35-40 kDa range (Fig. 7), two of which run as a doublet under different electrophoretic conditions (Fig. 6)] were undetectable in the supernatants of CS022, IB040, and CS451. These findings indicated that the presence of at least some of the products of the *prgHIJK* 25 operon were necessary for synthesis or secretion of *Ssp*.

The defect in bacterial mediated endocytosis associated with *prgH1::TnphoA* was complemented by a low-copy number plasmid, pWKSH5, containing a 5.1-kb fragment including *prgHIJK*, *org*, and *orf1*. Consistent 30 with this observation, the *prgH1::TnphoA* mutant carrying pWKSH5 (strain IB043) had a supernatant protein profile similar to that of wild type (Fig. 7). Of the five protein bands undetectable or greatly reduced in culture supernatants of *prgH1::TnphoA*, each was detected in IB043 35 and three of them were increased in amount (87 kDa, 65

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kDa, and 35 kDa) compared with wild-type supernatants. This finding demonstrates a correlation between the ability to secrete proteins and induction of epithelial cell bacterial mediated endocytosis.

5 The *prgH* locus is important for *S. typhimurium* to induce endocytosis by epithelial cells

The defect in BME of the *prgH1::TnphoA* mutant is complemented by a plasmid containing 5.1 kb of DNA from this region, indicating that the gene or genes disrupted 10 by the *prgH1::TnphoA* insertion are important for BME.

Analysis of the DNA sequence of this region identified six potential open reading frames that could be affected by this transposon insertion. As depicted in Fig. 1, five of these open reading frames, namely those 15 designated *prgH-K* are either disrupted (i.e., *prgH*) or are 3' to the *prgH1::TnphoA* insertion. The *orfl* translational start is 884 nucleotides upstream from the *TnphoA* insertion and that *orfl* is predicted to be oppositely transcribed from the *prgHIJK* operon.

20 An approximately 2600 nucleotide *PhoP*-repressed transcript was detected when RNA was hybridized with *prgH*-, *prgI-J*-, or *prgK*-specific DNA probes. In contrast, the predominant transcripts detected with *org* was smaller (approximately 1400 nucleotides), was not 25 altered in the *prgH1::TnphoA* mutant, and was not repressed by *PhoP*. Primer extension analysis of the potential start site of transcription, the size of the *prgHIJK* transcript, and the presence of a potential transcriptional terminator immediately downstream of *prgK* 30 also were consistent with transcription terminating before *org*.

In addition to the major transcripts of *prgHIJK* and *org*, a minor *PhoP*-repressed transcript of approximately 3800 nucleotides also was detected in 35 multiple RNA blots hybridized with the *org* and *prgH*,

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prgI-J, or *prgK* DNA probes. This minor RNA was similar in size to the combined *prgHIJK* and *org* open reading frames (i.e., 3731 nucleotides) and, thus, could represent cotranscription of *prgHIJK* and *org*. However, 5 both the 3800- and 1400-nucleotide transcripts were detected in RNA from the *prgH1::TnphoA* mutant suggesting that the 3800-nucleotide RNA did not represent cotranscription of *prgHIJK* and *org*. These data indicate that one or more genes in the *prgHIJK* operon are 10 important to BME of epithelial cells.

A *PhoP* constitutive mutation repressed the synthesis of approximately 20 *prg*-encoded cell-associated protein species (Miller et al., *J. Bacteriol.* 172:2485-2490, 1990, herein incorporated by reference). Although 15 *PhoP/PhoQ* has been shown to transcriptionally activate *pag* (Miller et al., *Proc. Natl. Acad. Sci. USA* 86:5054-5058, 1989, herein incorporated by reference; Pulkkinen et al., *supra*, herein incorporated by reference), the mechanism of protein repression by *PhoP/PhoQ* had not been 20 characterized prior to the present studies. No transcript was detected when RNA from the *PhoP* constitutive mutant was probed with *prgH-*, *prgI-J-*, or *prgK*-specific DNA, indicating that the *prgHIJK* operon was negatively regulated by *PhoP/PhoQ* at the level of 25 transcription. Thus, *PhoP/PhoQ* can both activate and repress transcription of virulence genes.

Consistent with the role of one or more of the products of *prgHIJK* in bacterial mediated endocytosis and possibly in protein secretion, a low-copy plasmid 30 containing 5.1 kb of DNA (IB043), including *prgHIJK*, *org*, and *orfl*, complemented both the bacterial mediated endocytosis defect and the supernatant protein profile defect of the *prgH1::TnphoA* mutant. Based upon its similarity to *MxiJ* and *YscJ*, which are 35 membrane-associated lipoproteins that are necessary for

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export and secretion of Ipa and Yops protein respectively, the *prgK* gene product is most likely to have such a role in bacterial mediated endocytosis and protein secretion. Similar to *PrgK*, *PrgH* was predicted 5 to be a membrane lipoprotein. However, in contrast to *prgI-K*, which are similar to plasmid-encoded genes of *Shigella* and *Yersinia* spp., a *prgH* DNA probe hybridized to chromosomal DNA but not virulence-plasmid DNA from *Shigella* spp.

10 Neither they nor the *prgI* or *prgJ* predicted gene products have signal sequences or long hydrophobic domains that suggest their cellular localization. However, the location of these genes within operons that encode secretion determinants suggests that they may have 15 a role in this process.

The predicted gene products of the *prgHIJK* operon were found to be similar to gene products required for protein secretion in other bacterial species. An analysis of proteins present in culture supernatants of 20 *S. typhimurium* was performed. These experiments revealed that the supernatants of wild-type cultures contained a large number of protein bands, whereas strains with mutations affecting the *prgH* locus, including *prgH1::TnphoA*, Δ *hil* and *PhoP^C* were each defective in 25 protein secretion as assessed by Ssp profiles. This analysis suggested that *PhoP/PhoQ* could control protein secretion, at least in part, by repressing *prgHIJK* whose products could form part of a secretion machinery. Furthermore, the finding that *PhoP^C* and Δ *hil* mutants were 30 associated with greater defects in their Ssp profile compared with the *prgH1::TnphoA* mutant suggested that more than one mechanism may be involved in protein secretion and that gene products encoded by the 10 kb region that is deleted in the *hil* mutant also contribute 35 to secretion of Ssp.

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Since the strains with altered Ssp profiles were each impaired in signaling epithelial cells, these data suggest that Ssp are involved in signaling such cells to initiate BME. The finding that five Ssp were missing 5 from culture supernatants of the *prgH* mutant suggested that one or more of these proteins were specifically involved in BME, e.g., Ssp and/or *prgHIJK* gene products may form a structure on the surface of *S. typhimurium* which induces bacterial mediated endocytosis.

10 *S. typhimurium* strains with transposons inserted between *prgH* and *spa* that result in reduced bacterial mediated endocytosis were also missing a subset of the Ssp missing from the *prgHIJK* mutant. DNA sequence analysis of the regions flanking the transposon 15 insertions revealed deduced protein sequences that were similar to *IpaB* and *IpaD* of *S. flexneri*. These data suggest that the transposon insertions define an operon in *S. typhimurium* that encodes Ipa homologues.

Example 2: *Salmonella typhimurium* Secreted Invasion

20 Determinants

Two *Salmonella typhimurium* secreted protein (Ssp) mutants with transposon insertions located between *spaT* and *prgH* were identified. One mutant lacks the 87 kDa Ssp, while the other lacks Ssp of 87, 42, and 36 kDa. 25 The invasiveness of these mutants implicates the 42 and 36 kDa Ssp, but not the 87 kDa Ssp in invasion. DNA sequencing of this region identified two complete and two partial open reading frames (designated *sspB*, *sspC*, *sspD*, and *sspA*).

30 The deduced amino acid sequences of *sspBCDA* are homologous to *Shigella flexneri* secreted proteins *IpaB*, *IpaC*, *IpaD*, and *IpaA*. Complementation analyses and amino-terminal sequencing showed that *sspC* and *sspA* encode the 42 kDa and the 87 kDa Ssp and that both

proteins are secreted without amino-terminal processing. SspA is abundantly secreted by wild type bacteria but is completely retained within the cellular fraction of a mutant in *prgHIJK* encoding part of the Ssp secretion apparatus. A precipitate containing SspC and three major Ssp of 63, 59, and 22 kDa was isolated from culture supernatants of wild type bacteria. These data indicate that major secreted invasion determinants of *S. typhimurium* are structurally and functionally homologous 10 to *S. flexneri* Ipa proteins.

The following reagents and experimental procedures were used to characterize Ssp.

Construction of plasmids and strains:

To construct pCH002, pVV8-1 was cut with *EcoRI*, 15 the 11 kb fragment eluted from a 1% agarose gel and cloned into the *EcoRI* site of pWSK29. In pCH002, transcription of *sspCDA* is driven from the *lac* promoter. pCH004 was constructed by cloning the 3 kb *BamHI* fragment from pCH002 into the *BamHI* site of pWSK29. pCH005 20 contains the 4 kb *EcoRI-PvuII* fragment from pCH002 cloned into *EcoRI-HincII* restricted pWSK29. pCH006 was constructed by restriction of pCH005 with *NcoI* and religation of the 1.7 kb and the 5 kb fragment. The correct orientations of the cloned inserts were confirmed 25 by appropriate restriction analyses.

PCR of a chromosomal fragment of EE638 comprising the 5'-region of *Tn51lacZY* and adjacent DNA was performed in three independent experiments by using primers OL 1 (5' CGCGGATCCATTATGGGATGTATCGG 3'; SEQ ID NO: 25) and 30 OL2 (5' CCGGCAGAAAATGTTGCAG 3'; SEQ ID NO: 26). The 0.8 kb amplified DNA fragments were then restricted with *BamHI* and cloned into pWSK29 for sequencing. All three sequences were identical.

Strain VB122 (*hilA::kan-112*) was constructed as 35 follows: the mutation was originally constructed on a

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plasmid by inserting a kan cassette (Pharmacia Biotech, Piscataway, NJ) in a *HincII* site in the 5' region of the *hilA* coding sequence. The plasmid-encoded *hilA::kan-112* mutation was recombined into the chromosome, and the 5 chromosomal mutation was confirmed by PCR analysis.

Mutant EE633 (*lacZY4*) was isolated by screening for oxygen regulated gene fusions created by random Tn5*lacZY* insertions in *S. typhimurium* VV114 (*hilA::kan-114*) and further selection for insertions 10 linked to a *hilA::kan-114* by P22 transduction into *S. typhimurium* SL1344 and selection for *Tet^R* and *Kan^R*.

Media and growth conditions for bacterial cultures:

Bacteria were grown in LB broth at 37°C. If 15 necessary, selection was carried out using 50 µg/ml ampicillin, 10 µg/ml tetracycline, or 25 µg/ml kanamycin.

Preparation and analysis of *S. typhimurium* supernatant proteins:

Bacterial cultures were grown for 16 to 17 hours 20 in 12 ml LB in 1.5 × 14 cm glass tubes at 37°C on a TC-7 roller (New Brunswick, Edison, NJ) at 50 rev./min. Soluble proteins from culture supernatants were obtained as described above. Precipitates in the culture were retrieved, rinsed 5 times with 1 ml H₂O, dissolved in 25 sample buffer (4% SDS, 12% glycerol, 5% β-mercaptoethanol, 0.05 M Tris-HCl pH 6.8, 0.01% bromphenol blue), and resolved in 10% polyacrylamide gels using SDS-PAGE and a Tris-Tricine buffer.

Immunoblotting:

30 Whole cell samples were prepared from overnight cultures using standard methods with the additional step of filtering the culture through a Whatman 1 qualitative paper filter (Whatman International, Maidstone, Kent, England) before centrifugation. The proteins were 35 resolved by SDS-PAGE and transferred to nitrocellulose by

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electroblotting using a conventional transfer buffer. Western blots were incubated with polyclonal rabbit serum prepared against the 87 kDa Ssp. The immunogen was purified by SDS-PAGE and injected into New Zealand White 5 rabbits (Charles River, Wilmington, MA). Serum was collected after two booster injections and subsequently absorbed with an acetone powder prepared from *S. typhimurium* strain EE63. Horseradish peroxidase-labelled goat anti-rabbit antibodies were used to label the 10 primary antibodies and were visualized using chemiluminescence (ECL, Amersham, International, Buckinghamshire, England)

Invasion assays:

Invasion of HEp-2 epithelial cells was carried out 15 according to the method of Behlau et al. (*J. Bacteriol.* 175:4475-4484, 1993). To minimize epithelial cell detachment from the bottom of the assay wells after bacterial uptake, the following modifications were introduced: invasion time was reduced from 90 to 60 min 20 and gentamicin treatment was performed for 15 min with 100 μ g/ml gentamicin, conditions which were shown to kill 99% of a bacterial culture of 2×10^8 cells/ml.

N-terminal protein sequencing:

Proteins separated by SDS-PAGE were blotted on 25 PVDF membranes (Bio-Rad, Hercules, CA) and stained with Ponceau-S. Blotted proteins were sequenced using an ABI 470A protein sequencer with 120A PTH-AA analyzer.

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Table 7: Strains and plasmids used in this example

	<u>Bacterial strain</u>	<u>Marker</u>
	<i>E. coli</i> DH5 α	F-Φ80dlacZ Δ M15 Δ (<i>lacZYA-argF</i>) U169endA1
		<i>recA1hsdR17</i> (r_K^- ,
5	m_K^+) <i>deoRthi-1supE44λgyrA96relA1</i>	
	<i>S. typhimurium</i> SL1344	wild type
	VV114	<i>hil</i> :: <i>kan-114</i>
	VB122	<i>Kan</i> ^R , <i>hilA</i> :: <i>kan-112</i>
10	EE637	<i>Tet</i> ^R , <i>invF</i> :: <i>lacZY11-5</i>
	EE633	<i>Tet</i> ^R , <i>sspA</i> :: <i>lacZY4</i>
	EE638	<i>Tet</i> ^R , <i>sspC</i> :: <i>lacZY11-6</i>
	<i>S. typhimurium</i> (ATCC14028s)	wild type
	CS451	14028s Δ <i>hil</i> :: <i>Tn5-428</i>
15	CS022	<i>pho-24</i> (<i>PhoP</i> ^C)
	IB04	<i>prgH1</i> :: <i>TnphoA</i>
	<u>Plasmid</u>	<u>Marker</u>
	pWSK29	<i>Amp</i> ^R
	pVV8-1	<i>Tet</i> ^R
20	pVV71	<i>Amp</i> ^R
	pCH002	<i>Amp</i> ^R , <i>sspCDA</i> , <i>hilA</i>
	pCH004	<i>Amp</i> ^R , <i>sspC</i>
	pCH005	<i>Amp</i> ^R , <i>sspCD</i>
	pCH006	<i>Amp</i> ^R , <i>sspD</i>

25 Identification of *S. typhimurium* Mutants with Transposon Insertions in Genes Encoding Ssp

To identify genes encoding Ssp, *Tn5lacZY* mutants of *S. typhimurium* SL1344 with transposon insertions located within the 40 kb "virulence island" (59-60 min. 30 of the *S. typhimurium* chromosome) were analyzed for changed patterns in Ssp. An insertion in *invF* (*invF*::*lacZY11-5*), the first gene of the *inv-spa* operon, and a *hilA*::*kan-112* insertion in VB122 led to major defects in the pattern of Ssp similar to a mutation in 35 the *prgHIJK* operon (*prgH1*::*TnphoA*) which has implicated in *S. typhimurium* protein secretion (see Example 1). Specifically, all three mutants lack 5 major Ssp of 36, 38, 42, 63 and 87 kDa, while the *hilA*::*kan-112* insertion leads to loss of some lower molecular weight protein 40 bands in addition to these 5 Ssp (Fig. 8, lanes 4, 5, 6).

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Two other mutants exhibited detectable loss of only one and of three Ssp, respectively. The supernatants from the mutant strain EE633 containing the fusion lacZY4 were missing a protein of 87 kDa, while supernatants from the 5 mutant strain EE638, containing fusion lacZY11-6, were missing protein species of 87, 42 and 36 kDa. In addition, supernatants from EE638 showed an increased abundance of a 63 kDa Ssp (Fig. 8, lanes 2, 3). Tn5lacZY in EE638 maps approximately 2.5 kb downstream from *spaT* 10 while in EE633 the transposon maps 5.5 kb downstream from *spaT* as determined by Southern hybridization and PCR analyses. Both transposons were inserted in the same orientation (Fig. 9). A degenerate pool of oligonucleotides synthesized according to the sequence of 15 the 12 amino-terminal amino acids of the 87 kDa protein (VTSVRTQPPVIM; SEQ ID NO: 27), hybridized specifically to a 5.5 kb BamHI fragment in pVV71 which comprises sequences between *hilA* and *spaT* (Fig. 9). These data indicate that the 87 kDa Ssp is encoded in the 20 chromosomal region adjacent to the transposon insertions. Tn5lacZY in EE633 is likely to be directly within the gene encoding the 87 kDa Ssp, while Tn5lacZY in EE638 is likely to be inserted within one of the genes encoding the 42 and the 36 kDa Ssp having a polar effect on the 25 synthesis of the other two Ssp missing in supernatants of this mutant.

Secretion of the 87 Ssp kDa Ssp is Dependent on *prgHIJK*

Since it was possible that the absence of the 87 kDa Ssp (Ssp87) in supernatants of EE633 and EE638 was 30 due to impaired secretion rather than expression, whole cell lysates and supernatants of various strains were analyzed by immunoblotting with antiserum raised against partially purified Ssp87. Fig. 11 shows that Ssp87 of wild type *S. typhimurium* is found mainly in the 35 supernatant, although some of the protein is detected in

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the cellular fraction (Fig. 11, lane 1). In contrast to wild type bacteria, all of the protein is found in the cellular fraction of the *prgH1::TnphoA* mutant IB040 (lane 3). *Ssp87* could not be detected in the cellular fractions nor in supernatants of various invasion and secretion mutants: CS022 (*PhoP^C*), a mutant which constitutively represses *PhoP* regulated genes (Miller et al., *J. Bacteriol.* 172:2485-2490, 1990, hereby incorporated by reference) (lane 2), CS451 (Δ*hil*::Tn5-428) carrying a 10 kb chromosomal deletion of the *hil* locus between 59 and 60 min. (lane 4), EE638 (*lacZY11-6*) (lane 5), and EE633 (*lacZY4*) (lane 6). The signal at 51 kDa in the supernatant fraction of wild type bacteria might represent a degradation product of *Ssp87*, while the faint band at 34 kDa is likely nonspecific hybridization since it is present in all bacteria analyzed. These results demonstrate that lack of *Ssp87* in supernatants of EE633 and EE638 is due to impaired expression while lack of *Ssp87* in supernatants of IB040 (*prgH1::TnphoA*) is caused by impaired secretion of the protein. These results further show that expression of the gene encoding *Ssp87* is affected by the *hil* deletion and that expression of *Ssp87*, either directly or indirectly, is repressed by *PhoP*.

25 Strain EE638, but not EE633, Is Markedly Deficient in Invasion

To determine the function of the 87, 42, and 36 kDa *Ssp* in invasion of epithelial cells, the ability of strain EE638 and EE633 to invade HEp-2 cells was analyzed. EE638 showed more than a 100-fold reduction in invasiveness when compared to wild type bacteria, while EE633 exhibited invasion levels comparable to wild type bacteria (Fig. 9). These results suggested that the 36 and/or the 42 kDa *Ssp* but not the 87 kDa *Ssp* are required for epithelial cell invasion. In addition, observation

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of interactions between these mutants and PtK2 cells by time-lapse videomicroscopy indicated that the ability of EE638 to induce epithelial cell membrane ruffling is also markedly reduced, while EE633 induced localized membrane 5 ruffles at a frequency similar to wild type *S. typhimurium*.

The Tn5lacZY Insertions in EE638 and EE633 Define a Chromosomal Region Encoding Ssp S. typhimurium Homologues of the Shigella ipaBCDA Operon

10 To determine the gene(s) affected by the transposon insertions in EE638 and EE633, part of a 11 kb EcoR1 subclone of pVV8-1 was sequenced. Two complete and two partial open reading frames (ORFs), positioned in the same transcriptional direction, were identified (Fig. 9).
15 The deduced gene products of the complete ORFs exhibit similarity to *Shigella* secreted proteins IpaC and IpaD (31% identity, 47% similarity; 37% identity, 56% similarity) respectively, and therefore were designated *sspC* and *sspD* (see Fig. 13 and Fig. 14). The gene
20 products of the complete open reading frames were designated *sspC* and *sspD*. The amino acid sequence derived from the 5'-end of *sspC* was identical to the amino-terminal sequence of the 42 kDa Ssp (underlined in Fig. 13). The deduced gene product of the partial ORF
25 located immediately upstream from *sspC* shows 47% identity (67% similarity) to the carboxyterminal portion of *S. flexneri* secreted protein IpaB and was designated *sspB* (Fig. 12). The ORF starting immediately downstream of *sspD* was designated *sspA*. The amino acid sequence
30 deduced from the 5' end of an ORF starting immediately downstream from *sspD* did not exhibit similarity to IpaA. However, DNA sequencing of internal parts of the gene predicted that the protein encoded by this gene, designated *sspA*, is similar to IpaA. Nevertheless, the
35 sequence of amino acids 2-13 (underlined in Fig. 15) was

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identical to the amino-terminal sequence of the 87 kDa Ssp (see above). *sspB*, *sspC*, *sspD*, and *sspA* are separated by 27, 70, and 15 bp, respectively, and putative ribosome binding sites precede *sspC*, *sspD*, and 5 *sspA*.

The amino acid similarities of Ssp to IpaB do not extend over the entire lengths of the proteins. The similarities between SspC/IpaC and SspD/IpaD are highest in the carboxy-terminal regions, while the central parts 10 of SspB and IpaB are conserved (see Fig. 12, 13, and 14). These similarities could reflect conservation in regions of the proteins required for secretion and/or invasion. Although both SspC and SspD appear to be secreted by the same mechanism, no obvious similarities or motifs common 15 to these proteins were detected, thus implying conformational rather than sequential features in the secretion of proteins by type III secretion pathways.

The precise insertion of Tn51lacZY in EE638 was determined by cloning and sequencing of a PCR product 20 comprising the 5' region of the transposon and upstream chromosomal sequences and was shown to be located 189 bp downstream from the ATG start codon of *sspC*. The order of the *ssp* genes and the Ssp profile of EE638 indicate that the transposon insertion in *sspC* is polar on 25 expression of *sspD* and *sspA* and that these genes are likely to be organized in a singly transcribed unit. Both *sspC* and *sspD* are Necessary for *S. typhimurium* Invasion of Epithelial Cells

A complementation analysis was carried out to 30 determine the minimal fragment necessary for complementation of the epithelial cell invasion defect of EE638 (*sspC::lacZY11-6*) as well as for reconstitution of Ssp. All analyzed fragments were cloned downstream from the lac promoter in the 6-8 copies/chromosome vector 35 pWSK29. As shown in Fig. 10, a 3.9 kb EcoRI-PvuII

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fragment comprising *sspC* and *sspD* in pCH005 was sufficient to complement the invasion defect of EE638 to wild type levels. When analyzed for Ssp, EE638 [pCH005] showed a pattern of Ssp similar to the wild type strain 5 [pWSK29] except for the missing 87 kDa protein (SspA) (Fig. 16, lane 4). EE638 transformed with pCH002 carrying an 11 kb *Eco*R1 fragment was partially complemented for invasion as well as for all 3 missing Ssp (Fig. 10 and Fig. 16, lane 6). In contrast, EE638 10 transformed with plasmids that contained either *sspC* or *sspD* alone (pCH004 and pCH006, respectively) were not complemented for invasion but showed reconstitution of the 42 kDa Ssp (SspC) or the 36 kDa Ssp (SspD), respectively (Fig. 10 and Fig. 16, lanes 3 and 5). In 15 addition, the abundance of a 63 kDa Ssp, which was found to be more abundant in supernatants of EE638, was reduced in supernatants of strains EE638 [pCH005], EE638 [pCH006], and EE638 [pCH002] and of SL1344 [pCH002]. These results demonstrate that both *SspC* and *SspD* are 20 necessary for invasion of epithelial cells and indicate that *SspC* encodes the 42 kDa Ssp while the 36 kDa Ssp is likely to be encoded by *SspD*. In addition, complementation of the invasion defect of EE638 with pCH005 indicates that invasiveness is not influenced by 25 the observed changes in the abundance of the 63 kDa Ssp.

A Precipitate Found in *S. typhimurium* Culture

Supernatants Contains Highly Abundant *SspC* and Other Proteins

Supernatants from *S. typhimurium* wild type 30 cultures contained a precipitate that, when solubilized in reducing SDS sample buffer, separates into at least four highly abundant protein bands of 63, 59, 42 and 22 kDa on SDS-PAGE (see Fig. 17, lane 1). Protein precipitates were also found in culture supernatants of 35 EE638 and EE633, but not in supernatants of *S.*

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typhimurium mutants with global defects in protein secretion [CS022 (PhoP^C), IB040 (prgH::TnphoA), CS451 (hil::Tn5-428) and VB122 (hilA::kan-112). S. typhimurium 14028s, the wild type parent of CS022 and 5 IB040, showed the same protein pattern of precipitated material as SL1344]. The precipitate from EE633 cultures showed a similar composition to that of wild type precipitate by SDS-PAGE analysis. In contrast, a major protein band of 42 kDa was absent from the precipitate 10 isolated from cultures of EE638 (Fig. 17, lane 2). Amino-terminal sequencing of this 42 kDa Ssp identified it as encoded by *SspC*. The identity of the amino-terminal protein sequence (MLISNVGINPAAAYLN; SEQ ID NO: 28) with the amino acid sequence derived from the 15 5'-region of *SspC* (Fig. 13) shows that no amino-terminal processing of *SspC* occurs prior to its release into the supernatant.

SDS-PAGE analyses of precipitated material from culture supernatants of EE638 [pCH004 (*SspC*)] and EE638 20 [pCH005 (*SspCD*)] showed a pattern similar to wild type [pWSK29] material (Fig. 17, lane 3 and 4), confirming that the respective plasmids complemented the mutant for secretion of *SspC*. Protein patterns of soluble Ssp and precipitates isolated from untransformed cultures of 25 SL1344 or EE638 were identical to those shown in Fig. 16, 17, lane 1 and 2, respectively. Precipitate of EE638 [pCH006 (*SspD*)] was found to be similar to precipitate from EE638 [pWSK29] except for reduced abundancy of a 63 kDa protein band (Fig. 17, lane 5). The precipitate from 30 EE638 [pCH002 (*SspCDA*)] contained an additional major protein band of approximately 51 kDa, which was also present in precipitate from SL1344 [pCH002] (Fig. 17, lanes 6, 7). Comparison of precipitated proteins to soluble Ssp on SDS-PAGE (Fig. 17, lanes 8, 9) showed that 35 *SspC* in the precipitate has the same electrophoretic

mobility as the 42 kDa soluble Ssp. These data suggest that the 42 kDa soluble Ssp is identical to precipitated SspC.

SspC and SspA are secreted proteins of 42 and 87 kDa, as demonstrated by amino-terminal sequencing and by complementation analyses. It is further likely that the 36 kDa protein encoded by *SspD* is secreted, since lack of a 36 kDa Ssp in supernatants of EE638 (*lacZY11-6*) was complemented by transformation of this mutant with 10 plasmids containing *SspD*. The 63 kDa Ssp is the protein likely to be encoded by SspB.

SspA, SspB, SspC, and SspD appear to be targets of the *inv-spa-prgHIJK* encoded secretion apparatus, since these Ssp are missing in supernatants of mutants 15 affecting expression or regulation of *inv-spa* and *prgHIJK* (Fig. 8). Typical for proteins secreted by type III secretion pathways, no amino-terminal processing of SspA and SspC was observed. The dependency of Ssp secretion on *prgHIJK* was further proven by demonstrating that SspA 20 is abundantly secreted by wild type cells, while it is completely retained in the cellular fraction of the *prgH1* ::*TnphoA* mutant IB040 (Fig. 11). The 38 kDa Ssp of the five major Ssp dependent on the *inv-spa-prgHIJK* secretion apparatus may be the product of the *invJ* invasion locus.

25 The immunoblot analysis of SspA secretion suggests that expression of the gene encoding SspA is negatively controlled by the virulence two component regulatory system PhoP/PhoQ. PhoP/Q has a global effect on protein secretion which is partially due to negative 30 transcriptional regulation of *prgHIJK* (see Example 1).

The SspBCDA genes are located between the large *inv-spa* gene cluster and *prgHIJK* at 59 minutes on the *S. typhimurium* chromosome. Fig. 18 shows the relative positions of the invasion genes in *S. typhimurium* in 35 comparison to their *S. flexneri* homologues, which are

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clustered in a 31 kb region of a large virulence plasmid. The invasion genes cluster in three groups (*inv-spa/mxi-spa*, *Ssp/ipa*, and *prgIJK/mxiHIJ*) which exhibit conserved gene structure and organization, 5 suggesting that these genes were acquired by horizontal gene transfer. Acquisition by horizontal gene transfer is further supported by the fact that these *S. typhimurium* invasion genes are within a 40 kb "virulence island" which, despite the otherwise high overall genetic 10 similarity between *S. typhimurium* and *E. coli* K-12, is unique to *S. typhimurium*. However, the three invasion gene clusters from *S. flexneri* and *S. typhimurium* are in different relative positions to each other and are interspersed between non-homologous genes, thus implying 15 multi-recombinational events in the evolution of these genetic regions.

In addition to soluble *Ssp* the supernatants of *S. typhimurium* cultures contained a flocculent precipitate consisting of *SspC* and three other major protein species 20 of 63 (*Ssp* 63), 59 (*Ssp* 59), and 22 (*Ssp* 22) kDa. The combination and abundancy of *Ssp* in the precipitate from *S. typhimurium* cultures is strikingly different from that in the soluble fraction (see Fig. 17). Though *Ssp*, including *SspC*, are found in both the precipitate and the 25 soluble fraction, *SspD*, even when overproduced, was not detected in the precipitate. This emphasizes the difference in composition of precipitate and soluble fraction and supports the possibility of specific protein-protein interactions between the four *Ssp* leading 30 to precipitate formation.

OTHER EMBODIMENTS

Using reagents derived from partial cDNA clones of an *Ssp*, e.g., *SspA*, the isolation of a full-length cDNA encoding the *Ssp* is well within the skill of those

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skilled in the art of molecular biology. For example, a radiolabelled probe made from a known partial cDNA sequence can be used to identify and isolate from a library of recombinant plasmids cDNAs that contain 5 regions with identical to the previously isolated cDNAs. The screening of cDNA libraries with radiolabelled cDNA probes is routine in the art of molecular biology (see Sambrook et al., 1989, *Molecular Cloning: a Laboratory Manual*, second edition., Cold Spring Harbor Press, Cold 10 Spring Harbor, N.Y.). The cDNA can be isolated and subcloned into a plasmid vector, and the plasmid DNA purified by standard techniques. The cDNA insert is sequenced using the dideoxy chain termination method well known in the art (Sambrook et al, *supra*). 15 Oligonucleotide primers corresponding to bordering vector regions as well as primers prepared from previously isolated cDNA clones can be employed to progressively determine the sequence of the entire gene.

Similar methods can be used to isolate Ssp which 20 are related to SspA, SspB, SspC, or SspD. To isolate related Ssp, a probe having a sequence derived from (or identical to) all or a portion of SspA, SspB, SspC, or SspD can be used to screen a library of *Salmonella* DNA (or cDNA). DNA encoding a related Ssp will generally 25 hybridize at greater stringency than DNA encoding other proteins. This approach can be used to identify *Salmonella typhimurium* Ssp as well as Ssp of other *Salmonella*.

Generation of Monoclonal Antibodies:

30 Monoclonal antibodies can be generated to purified native or recombinant gene products, e.g., Ssp, by standard procedures, e.g., those described in Coligan et al., eds., *Current Protocols in Immunology*, 1992, Greene Publishing Associates and Wiley-Interscience). To 35 generate monoclonal antibodies, a mouse is immunized with

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the recombinant protein, and antibody-secreting B cells isolated and immortalized with a non-secretory myeloma cell fusion partner. Hybridomas are then screened for production of specific antibodies and cloned to obtain a 5 homogenous cell population which produces a monoclonal antibody. For example, hybridomas secreting the desired antibodies can be screened by ELISA. Specificities of the monoclonal antibodies can be determined by the use of different protein or peptide antigens in the ELISA.

10 Useful quantities of antibodies can be produced by either the generation of ascites fluid in mice or by large scale *in vitro* culture of the cloned antibody-producing hybridoma cell line. Antibodies can be purified by various chromatographic procedures known in the art, such 15 as affinity chromatography on either immobilized Protein A or Protein G.

The invention also includes DNA encoding other Ssp (e.g., Ssp 54, Ssp 42, and Ssp 22) found in cell supernatants. Those skilled in the art can readily clone 20 the corresponding genes based on the amino terminal sequence or the corresponding protein. The amino terminal sequence of Ssp54 is MNNLTLSXFXKVG (SEQ ID NO: 29). The amino terminal sequence of Ssp42 is 25 MLISNVGINPAAAYLN (SEQ ID NO: 30). The amino terminal sequence of Ssp 22 is TKITLSPQNFFI (SEQ ID NO: 31).